Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-32. (Canceled).

33. (Currently amended) A method for identifying candidate therapeutic agents for the treatment of prostate cancer, the method comprising:

(a) obtaining a test sample comprising prostate tumor cells encoding a protein having the amino acid sequence of SEQ ID NO:2;

(b) exposing the test sample to a test compound;

(c) measuring the level of expression of alpha-methylacyl-CoA racemase mRNA comprising the nucleotide sequence of SEQ ID NO:3 wherein a U is substituted for each T in the test sample exposed to the test compound; and

(d) identifying the test compound as a candidate therapeutic agent for the treatment of prostate cancer if the level of expression of alpha-methylacyl-CoA racemase mRNA in the test sample exposed to the test compound is less than in a control test sample not exposed to the test compound.

34. (Previously presented) The method of claim 33 wherein step (c) comprises exposing the test sample to a nucleic acid probe which hybridizes to a nucleic acid molecule consisting of SEQ ID NO:3 under hybridization in 0.5M sodium phosphate, 7% SDS at 65°C, followed by one or more washes at 0.2X SSC, 1% SDS at 65°C, wherein the nucleic acid probe comprises a fragment of the full-length complement of SEQ ID NO:3.

35-58. (Canceled).

59. (Previously presented) The method of claim 34 wherein step (c) comprises contacting alpha-methylacyl-CoA racemase mRNA with a nucleic acid probe comprising a fragment of the full-length complement of SEQ ID NO:3 the fragment comprising at least 15 consecutive nucleotides of the full-length complement of SEQ ID NO:3.

60. (Previously presented) The method of claim 59 wherein the probe comprises at least 20 consecutive nucleotides of the full-length complement of SEQ ID NO:3.

61. (Previously presented) The method of claim 59 wherein the probe comprises at least 25 consecutive nucleotides of the full-length complement of SEQ ID NO:3.

62. (Previously presented) The method of claim 59 wherein the probe comprises at least 30 consecutive nucleotides of the full-length complement of SEQ ID NO:3.

63. (Previously presented) The method of claim 59 wherein the probe comprises at least 40 consecutive nucleotides of the full-length complement of SEQ ID NO:3.

64. (Previously presented) The method of claim 59 wherein the probe comprises at least 50 consecutive nucleotides of the complement of SEQ ID NO:3.

65. (Previously presented) The method of claim 59 wherein the probe comprises at least 75 consecutive nucleotides of the full-length complement of SEQ ID NO:3.

66. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 260 nucleotides.

67. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 300 nucleotides.

68. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 400 nucleotides.

69. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 500 nucleotides.

70. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 800 nucleotides.

71. (Previously presented) The method of claim 34 wherein the nucleic acid probe comprises at least 900 nucleotides.

72. (Currently amended) The method of claim 34 wherein the nucleic acid probe comprises at least [900] 1000 nucleotides.

73. (Previously presented) The method of claim 59 wherein the probe is immobilized on a surface.

74. (Previously presented) The method of claim 34 wherein the alpha-methylacyl-CoA racemase mRNA is immobilized on a surface.

75. (Previously presented) The method of claim 33 wherein step (c) comprises amplification of the alpha-methylacyl-CoA racemase mRNA.

76. (Previously presented) The method of claim 59 wherein the probe is detectably labeled.

77. (Previously presented) The method of claim 76 wherein the detectable label is selected from the group consisting of a chemiluminescent label, a fluorescent label, a radioactive label, or a colorimetric label.

78. (Previously presented) The method of claim 34 wherein the probe is detectably labeled.

79. (Previously presented) The method of claim 78 wherein the detectable label is selected from the group consisting of a chemiluminescent label, a fluorescent label, a radioactive label, or a colorimetric label.